To: Peter Israelsson[pisraelsson@anchorqea.com]; Peter Oates[poates@anchorqea.com]
Cc: Garland, Edward[Edward.Garland@hdrinc.com]; Vaughn, Stephanie[Vaughn.Stephanie@epa.gov]; Kirchner, Scott[KirchnerSF@cdmsmith.com]; Naranjo, Eugenia[Naranjo.Eugenia@epa.gov]
From: Wands, James
Sent: Thur 2/12/2015 4:59:29 PM
Subject: RE: Particle mixing rate question

Peter and Pete,

I just wanted to touch base with you guys on a couple of items.

1) I am still having trouble locating the spreadsheets with the correct version of the partitioning calculation from CARP used to generate the inputs to the model. There were many versions that were worked on by multiple individuals ~9 years ago. I apologize that I have not been able to find the correct version yet.

2) I have a concern with the fluff layer averaging in the model. I appreciate the idea behind the depth averaging, but what about a case where the fluff layer is only present for a brief time. The depth weighted average would carry a depth weighted average concentration from the time the layer was present over the entire averaging period, and the bioaccumulation model will not see that that concentration was not present for most of the averaging period, it will simply see the concentration. Please see the simplified example below. Any thoughts on how to address this?

3) Is it the case that the dissolved and particulate phases are never calculated in the fluff layer in the code?

4) Is it also the case that there is no diffusive and particle mixing exchange between the fluff layer and the water column or bedded sediments?

5) The only fluff layer interactions are deposition into fluff layer from the water column, erosion from the fluff layer to the water column, and deposition from the fluff layer to the bed, correct?

6) Diffusion occurs between the top layer of the bedded sediment and the water column with no interaction with the fluff, correct?

Fluff Layer averaging:

Hour	Concentration	Thickness	C*H	Cumulative C*H	Cumulative H
1	1	1	1	1	1
2	1	0.5	0.5	1.5	1.5
3	1	0.25	0.25	1.75	1.75
4	0	0	0	1.75	1.75
5	0	0	0	1.75	1.75

6	0	0	0	1.75	1.75
7	0	0	0	1.75	1.75
8	0	0	0	1.75	1.75
9	0	0	0	1.75	1.75
10	0	0	0	1.75	1.75
11	0	0	0	1.75	1.75
12	0	0	0	1.75	1.75
13	0	0	0	1.75	1.75
14	0	0	0	1.75	1.75
15	0	0	0	1.75	1.75
16	0	0	0	1.75	1.75
17	0	0	0	1.75	1.75
18	0	0	0	1.75	1.75
19	0	0	0	1.75	1.75
20	0	0	0	1.75	1.75
21	0	0	0	1.75	1.75
22	0	0	0	1.75	1.75
23	0	0	0	1.75	1.75
24	0	0	0	1.75	1.75

Average	1	0.072917

Thanks,

James

From: Wands, James
Sent: Wednesday, January 21, 2015 11:56 AM
To: Peter Israelsson; Peter Oates
Cc: Garland, Edward (Edward.Garland@hdrinc.com); Vaughn, Stephanie (Vaughn.Stephanie@epa.gov); Kirchner, Scott
Subject: Particle mixing rate question

Peter, Pete,

I am looking at the particle mixing in the contaminant model runs that we received in December. I see that you have implemented 3D particle mixing rates in the bed and the implementation in the code appears to work correctly. I had a question about the input parameterization for the mixing rate. Looking at the inputs it appears there are two distinct profiles for vertical mixing in the model runs we are looking at. Both are identical below 2 cm. One has the highest mixing at the surface and the other has zero mixing at the surface. In the attached figure there is a map on the left with model grid cells colored either red or blue, the center panel has the mixing rate plotted verses depth on an arithmetic scale, and the panel on the right is the same information repeated on a log scale axis. The color on the map indicates the profile used at that location. The red cells are locations where there is no mixing in the top 2 centimeters. You will have to zoom in to see some areas.

Is there a justification for zero mixing at the surface in the red cells, or is this potentially a mistake in the input deck?

Thanks,

James

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